

1642

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/716,928A

DATE: 08/21/2002
 TIME: 15:14:25

Input Set : A:\GI-20.txt
 Output Set: N:\CRF4\08212002\I716928A.raw

3 <110> APPLICANT: Dunussi-Joannopoulos, Kyriaki
 5 <120> TITLE OF INVENTION: USE OF COMBINATION THERAPY COMPRISING A STIMULATORY
 6 FORM OF A COSTIMULATORY MOLECULE AND A CHEMOTHERAPEUTIC
 7 AGENT
 9 <130> FILE REFERENCE: GNN-020
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/716,928A
 12 <141> CURRENT FILING DATE: 2000-11-20
 14 <150> PRIOR APPLICATION NUMBER: USSN 60/247,329
 15 <151> PRIOR FILING DATE: 2000-11-10
 17 <160> NUMBER OF SEQ ID NOS: 12
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1491
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (318)..(1181)
 30 <220> FEATURE:
 31 <221> NAME/KEY: mat_peptide
 32 <222> LOCATION: (420)
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: Open reading frame from location 318 to 1181 bp
 37 <220> FEATURE:
 38 <223> OTHER INFORMATION: Alternate polyadenylation signal from location
 39 1474 to 1479 bp
 41 <400> SEQUENCE: 1
 42 ccaaagaaaa agtggattgt cattgctta tagactgtaa gaagagaaca ttcagaatgt 60
 44 ggagtcttac cctgaaatca aaggatttaa agaaaaatgt gaatttttct tcagaagct 120
 46 gtgaaactaa atccacaacc ttggagacc caggaacacc ctccatctc tgtgtgttt 180
 48 gtaaacatca ctggagggtc ttctacgtga gcaattggat tgtcatcgc cctgcctgtt 240
 50 ttgcacctgg gaagtgcctt ggtttactt ggtccaaat tggtggctt cactttgac 300
 52 cctaagcattc tgaagcc atg ggc cac aca cgg agg cag gga aca tca cca 350
 53 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
 54 -30 -25
 56 tcc aag tgt cca tac ctg aat ttc ttt cag ctc ttg gtg ctg gct ggt 398
 57 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
 58 -20 -15 -10
 60 ctt tct cac ttc tgt tca ggt gtt atc cac gtg acc aag gaa gtg aaa 446
 61 Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys
 62 -5 -1 1 5
 64 gaa gtg gca acg ctg tcc tgt ggt cac aat gtt tct gtt gaa gag ctg 494
 65 Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Leu

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66	10	15	20	25														
68	gca	caa	act	cgc	atc	tac	tgg	caa	aag	gag	aag	aaa	atg	gtg	ctg	act	542	
69	Ala	Gln	Thr	Arg	Ile	Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr		
70					30				35				40					
72	atg	atg	tct	ggg	gac	atg	aat	ata	tgg	ccc	gag	tac	aag	aac	cgg	acc	590	
73	Met	Met	Ser	Gly	Asp	Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr		
74					45				50				55					
76	atc	ttt	gat	atc	act	aat	aac	ctc	tcc	att	gtg	atc	ctg	gct	ctg	cgc	638	
77	Ile	Phe	Asp	Ile	Thr	Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg		
78					60				65				70					
80	cca	tct	gac	gag	ggc	aca	tac	gag	tgt	gtt	ctg	aag	tat	gaa	aaa		686	
81	Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys		
82					75				80				85					
84	gac	gct	ttc	aag	cgg	gaa	cac	ctg	gct	gaa	gtg	acg	tta	tca	gtc	aaa	734	
85	Asp	Ala	Phe	Lys	Arg	Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys		
86					90				95				100				105	
88	gct	gac	ttc	cct	aca	cct	agt	ata	tct	gac	ttt	gaa	att	cca	act	tct	782	
89	Ala	Asp	Phe	Pro	Thr	Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser		
90					110				115				120					
92	aat	att	aga	agg	ata	att	tgc	tca	acc	tct	gga	ggt	ttt	cca	gag	cct	830	
93	Asn	Ile	Arg	Arg	Ile	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro		
94					125				130				135					
96	cac	ctc	tcc	tgg	ttg	gaa	aat	gga	gaa	tta	aat	gcc	atc	aac	aca		878	
97	His	Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr		
98					140				145				150					
100	aca	gtt	tcc	caa	gat	cct	gaa	act	gag	ctc	tat	gct	gtt	agc	agc	aaa	926	
101	Thr	Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys		
102					155				160				165					
104	ctg	gat	ttc	aat	atg	aca	acc	aac	cac	agc	ttc	atg	tgt	ctc	atc	aag	974	
105	Leu	Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys		
106					170				175				180				185	
108	tat	gga	cat	tta	aga	gtg	aat	cag	acc	ttc	aac	tgg	aat	aca	acc	aag	1022	
109	Tyr	Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys		
110					190				195				200					
112	caa	gag	cat	ttt	cct	aat	acc	ctg	ctc	cca	tcc	tgg	gcc	att	acc	tta	1070	
113	Gln	Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu		
114					205				210				215					
116	atc	tca	gta	aat	gga	att	ttt	gtg	ata	tgc	tgc	ctg	acc	tac	tgc	ttt	1118	
117	Ile	Ser	Val	Asn	Gly	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe		
118					220				225				230					
120	gcc	cca	aga	tgc	aga	gag	aga	agg	aat	gag	aga	ttg	aga	agg	gaa		1166	
121	Ala	Pro	Arg	Cys	Arg	Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu		
122					235				240				245					
124	agt	gta	cgc	cct	gta	taacagtgtc	cgcagaagca	aggggctgaa	aagatctgaa								1221	
125	Ser	Val	Arg	Pro	Val													
126	250																	
128	ggtagcctcc	gtc	atc	tct	tt	ggggataaca	tggatcg	tgg	ggatcat	gag	gcatt	cttcc	1281					
130	cttaacaat	tta	agctgtt	tt	acc	acta	cct	cac	ctt	taaaaac	ct	ttc	ag	1341				
132	aagctgaaca	gtt	aca	agat	gg	ctggc	atc	c	ctt	ccat	ttt	ctccccat	at	gca	attt	gct	1401	

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134 taatgttaacc tcttctttg ccatgtttcc attctgccat cttgaattgt cttgtcagcc 1461
 136 aattcattat ctattaaaca ctaatttgag 1491
 139 <210> SEQ ID NO: 2
 140 <211> LENGTH: 288
 141 <212> TYPE: PRT
 142 <213> ORGANISM: Homo sapiens
 144 <400> SEQUENCE: 2
 145 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
 146 -30 -25 -20
 148 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
 149 -15 -10 -5
 151 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
 152 -1 1 5 10
 154 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
 155 15 20 25 30
 157 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
 158 35 40 45
 160 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
 161 50 55 60
 163 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
 164 65 70 75
 166 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
 167 80 85 90
 169 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
 170 95 100 105 110
 172 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
 173 115 120 125
 175 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
 176 130 135 140
 178 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
 179 145 150 155
 181 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
 182 160 165 170
 184 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
 185 175 180 185 190
 187 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
 188 195 200 205
 190 Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
 191 210 215 220
 193 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
 194 225 230 235
 196 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
 197 240 245 250
 200 <210> SEQ ID NO: 3
 201 <211> LENGTH: 1120
 202 <212> TYPE: DNA
 203 <213> ORGANISM: Homo sapiens
 205 <220> FEATURE:
 206 <221> NAME/KEY: CDS

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207 <222> LOCATION: (107)..(1093)
 209 <400> SEQUENCE: 3
 210 cacagggtga aagcttgct tctctgctgc tgtaacaggg actagcacag acacacggat 60
 212 gagtggttgc atttccagat attaggtcac agcagaagca gccaaa atg gat ccc 115
 213 Met Asp Pro
 214 1
 216 cag tgc act atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg 163
 217 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
 218 5 10 15
 220 ctc tct ggt gct gct cct ctg aag att caa gct tat ttc aat gag act 211
 221 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
 222 20 25 30 35
 224 gca gac ctg cca tgc caa ttt gca aac tct caa aac caa agc ctg agt 259
 225 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
 226 40 45 50
 228 gag cta gta gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag 307
 229 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
 230 55 60 65
 232 gta tac tta ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg 355
 233 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
 234 70 75 80
 236 ggc cgc aca agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat 403
 237 Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
 238 85 90 95
 240 ctt cag atc aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa 451
 241 Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
 242 100 105 110 115
 244 aag ccc aca gga atg att cgc atc cac cag atg aat tct gaa ctg tca 499
 245 Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
 246 120 125 130
 248 gtg ctt gct aac ttc agt caa cct gaa ata gta cca att tct aat ata 547
 249 Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile
 250 135 140 145
 252 aca gaa aat gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac 595
 253 Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr
 254 150 155 160
 256 cca gaa cct aag aag atg agt gtt ttg cta aga acc aag aat tca act 643
 257 Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr
 258 165 170 175
 260 atc gag tat gat ggt att atg cag aaa tct caa gat aat gtc aca gaa 691
 261 Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu
 262 180 185 190 195
 264 ctg tac gac gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg 739
 265 Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr
 266 200 205 210
 268 agc aat atg acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt 787
 269 Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu
 270 215 220 225
 272 tta tct tca cct ttc tct ata gag ctt gag gac cct cag cct ccc cca 835

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273	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	
274	230				235				240								
276	gac	cac	att	cct	tgg	att	aca	gct	gta	ctt	cca	aca	gtt	att	ata	tgt	883
277	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	
278	245				250				255								
280	gtg	atg	gtt	ttc	tgt	cta	att	cta	tgg	aaa	tgg	aag	aag	aag	aag	cgg	931
281	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	
282	260			265				270								275	
284	cct	cgc	aac	tct	tat	aaa	tgt	gga	acc	aac	aca	atg	gag	agg	gaa	gag	979
285	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	
286	280			285				290									
288	agt	gaa	cag	acc	aag	aaa	aga	gaa	aaa	atc	cat	ata	cct	gaa	aga	tct	1027
289	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	
290	295			300				305									
292	gat	gaa	gcc	cag	cgt	gtt	ttt	aaa	agt	tcg	aag	aca	tct	tca	tgc	gac	1075
293	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	
294	310			315				320									
296	aaa	agt	gat	aca	tgt	ttt	taattaaaga	gtaaaagccca	aaaaaaa								1120
297	Lys	Ser	Asp	Thr	Cys	Phe											
298	325																
301	<210>	SEQ	ID	NO:	4												
302	<211>	LENGTH:	329														
303	<212>	TYPE:	PRT														
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308	1			5				10								15	
310	Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe	
311		20			25			30									
313	Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln	
314		35			40			45									
316	Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	
317		50			55			60									
319	Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	
320		65			70			75								80	
322	Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	
323			85			90			95								
325	Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	
326			100			105			110								
328	His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	
329		115			120			125									
331	Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	
332		130			135			140									
334	Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	
335		145			150			155								160	
337	His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	
338			165			170			175								
340	Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	
341			180			185			190								

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number